



Research Conducted by OIR Could Help Refine the Molecular Classification of Lymphoma

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Recently published research in the New England Journal of Medicine could lead to the creation of more targeted therapies and more accurate prognoses for patients with diffuse large B-cell lymphoma (DLBCL).

Investigators working on the [study](#) performed a multi-platform analysis of genomic alterations and gene expression on tumor samples from 574 patients with DLBCL, according to the [press release](#) issued by the National Cancer Institute (NCI). The results from this analysis indicated that two genetic subtypes, BN2 and EZB, respond well to the standard treatment for DLBCL while two subtypes, MCD and N1, do not.

Dr. Calvin A. Johnson, Chief of the High Performance Computing Informatics Office (HPCIO), spoke about the significant role his group played in this study. "Working closely with Dr. Louis Staudt's lab at the National Cancer Institute, we developed and adapted machine learning models to perform predictive analytics on DLBCL cancer genomic data," he said.

Dr. Johnson described how his staff used random forest algorithms and support vector machines, [supervised learning methods](#), to advance knowledge in cancer genomics. In machine learning, supervised learning methods involve researchers training an algorithm to identify patterns in data by appropriately labeling sample data. "We trained a random forest to corroborate the core finding, the discovery of four genetic subtypes. We also devised specialized models to discern somatic from germline variants and to predict novel somatic hypermutations in the data."

The OIR researchers who contributed to the study included Dr. Calvin A. Johnson, Dr. Sophie Du, Bin Zhou, and Jeff Liu.